

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 08/894,3560
Source: IFW/6
Date Processed by STIC: 10/11/05

ENTERED



IFW16

RAW SEQUENCE LISTING
 PATENT APPLICATION: **US/08/894,356D**

DATE: 10/11/2005
 TIME: 08:45:08

Input Set : **A:\72370308.app**
 Output Set: **N:\CRF4\10112005\H894356D.raw**

3 <110> APPLICANT: ASHIKARI, TOSHIHIKO
 4 TANAKA, YOSHIKAZU
 5 FUJIWARA, HIROYUKI
 6 NAKAO, MASAHIRO
 7 FUKUI, YUKO
 8 SAKAKIBARA, KEIKO
 9 MIZUTANI, MASAKO
 10 KUSUMI, TAKAAKI
 12 <120> TITLE OF INVENTION: A GENE ENCODING A PROTEIN HAVING ACYL GROUP TRANSFER
 13 ACTIVITY
 15 <130> FILE REFERENCE: 47237-0308/US
 17 <140> CURRENT APPLICATION NUMBER: 08/894,356D
 18 <141> CURRENT FILING DATE: 1997-08-18
 20 <150> PRIOR APPLICATION NUMBER: JP 7-67159
 21 <151> PRIOR FILING DATE: 1995-02-17
 23 <150> PRIOR APPLICATION NUMBER: JP 7-196915
 24 <151> PRIOR FILING DATE: 1995-06-29
 26 <150> PRIOR APPLICATION NUMBER: JP 8-46534
 27 <151> PRIOR FILING DATE: 1996-01-30
 29 <150> PRIOR APPLICATION NUMBER: PCT/JP96/00348
 30 <151> PRIOR FILING DATE: 1996-02-16
 32 <160> NUMBER OF SEQ ID NOS: 40
 34 <170> SOFTWARE: PatentIn Ver. 3.3
 36 <210> SEQ ID NO: 1
 37 <211> LENGTH: 1703
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Gentiana triflora
 41 <220> FEATURE:
 42 <221> NAME/KEY: CDS
 43 <222> LOCATION: (6)..(1412)
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 48 1 5 10 15
 50 aca cca cca tct gac aca aca gat gtc gag tta tcg cta ccg gta aca 98
 51 Thr Pro Pro Ser Asp Thr Asp Val Glu Leu Ser Leu Pro Val Thr
 52 20 25 30
 54 ttc ttc gat atc ccc tgg ttg cac ttg aat aag atg cag tcc ctt ctg 146
 55 Phe Phe Asp Ile Pro Trp Leu His Leu Asn Lys Met Gln Ser Leu Leu
 56 35 40 45
 58 ttt tac gac ttt ccg tac cca aga aca cat ttc ttg gac act gtt atc 194
 59 Phe Tyr Asp Phe Pro Tyr Pro Arg Thr His Phe Leu Asp Thr Val Ile
 60 50 55 60

P.6

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63	Pro	Asn	Leu	Lys	Ala	Ser	Leu	Ser	Leu	Thr	Leu	Lys	His	Tyr	Val	Pro	
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67	Leu	Ser	Gly	Asn	Leu	Leu	Met	Pro	Ile	Lys	Ser	Gly	Glu	Met	Pro	Lys	
68	80						85			90		95					
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71	Phe	Gln	Tyr	Ser	Arg	Asp	Glu	Gly	Asp	Ser	Ile	Thr	Leu	Ile	Val	Ala	
72	100						105			105		110					
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75	Glu	Ser	Asp	Gln	Asp	Phe	Asp	Tyr	Leu	Lys	Gly	His	Gln	Leu	Val	Asp	
76	115						120			125							
78	tcc	aat	gat	ttg	cat	ggc	ctt	ttt	tat	gtt	atg	cca	ccg	gtt	ata	agg	434
79	Ser	Asn	Asp	Leu	His	Gly	Leu	Phe	Tyr	Val	Met	Pro	Arg	Val	Ile	Arg	
80	130						135			140							
82	acc	atg	caa	gac	tat	aaa	gtg	atc	ccg	ctc	gta	gcc	gtg	caa	gta	acc	482
83	Thr	Met	Gln	Asp	Tyr	Lys	Val	Ile	Pro	Leu	Val	Ala	Val	Gln	Val	Thr	
84	145						150			155							
86	gtt	ttt	cct	aac	cgt	ggc	ata	gcc	gtg	gct	ctg	acg	gca	cat	cat	tca	530
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88	160						165			170		175					
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106	gga	agc	aaa	ccc	cct	cga	ttc	aac	aag	gta	cga	gct	aca	tat	gtc	ctc	770
107	Gly	Ser	Lys	Pro	Pro	Arg	Phe	Asn	Lys	Val	Arg	Ala	Thr	Tyr	Val	Leu	
108	240						245			250		255					
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111	Ser	Leu	Ala	Glu	Ile	Gln	Lys	Leu	Lys	Asn	Lys	Val	Leu	Asn	Leu	Arg	
112	260						265			265		270					
114	gga	tcc	gaa	ccg	aca	ata	cgt	gta	acg	acg	ttc	aca	atg	acg	tgt	gga	866
115	Gly	Ser	Glu	Pro	Thr	Ile	Arg	Val	Thr	Thr	Phe	Thr	Met	Thr	Cys	Gly	
116	275						280			280		285					
118	tac	gta	tgg	aca	tgc	atg	gtc	aaa	tca	aaa	gat	gac	gtc	gta	tca	gag	914
119	Tyr	Val	Trp	Thr	Cys	Met	Val	Lys	Ser	Lys	Asp	Asp	Val	Val	Ser	Glu	
120	290						295			300							
122	gaa	tca	tcg	aac	gac	gaa	aat	gag	ctc	gag	tac	ttc	agt	ttt	aca	gcg	962
123	Glu	Ser	Ser	Asn	Asp	Glu	Asn	Glu	Leu	Glu	Tyr	Phe	Ser	Phe	Thr	Ala	
124	305						310			315							
126	gat	tgc	cga	gga	ctt	ctg	acg	ccc	ccg	tgt	cct	aac	tac	ttt	ggc		1010

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130	aac	tgt	ctt	gcg	tca	tgc	gtt	gca	aaa	gca	aca	cat	aaa	gag	tta	gtt	1058		
131	Asn	Cys	Leu	Ala	Ser	Cys	Val	Ala	Lys	Ala	Thr	His	Lys	Glu	Leu	Val			
132						340				345						350			
134	ggg	gat	aaa	ggg	ctt	ctt	gtt	gca	gct	att	gga	gaa	gcc	att			1106		
135	Gly	Asp	Lys	Gly	Leu	Leu	Val	Ala	Val	Ala	Ala	Ile	Gly	Glu	Ala	Ile			
136						355				360						365			
138	gaa	aag	agg	ttg	cac	aac	gaa	aaa	ggc	gtt	ctt	gca	gat	gca	aaa	act	1154		
139	Glu	Lys	Arg	Leu	His	Asn	Glu	Lys	Gly	Val	Leu	Ala	Asp	Ala	Lys	Thr			
140						370				375						380			
142	tgg	tta	tcg	gaa	tct	aat	gga	atc	cct	tca	aaa	aga	ttt	ctc	ggg	att	1202		
143	Trp	Leu	Ser	Glu	Ser	Asn	Gly	Ile	Pro	Ser	Lys	Arg	Phe	Leu	Gly	Ile			
144						385				390						395			
146	acc	gga	tcg	cct	aag	ttc	gat	tcg	tat	ggt	gta	gat	ttt	gga	tgg	gga	1250		
147	Thr	Gly	Ser	Pro	Lys	Phe	Asp	Ser	Tyr	Gly	Val	Asp	Phe	Gly	Trp	Gly			
148						400				405						410	415		
150	aag	cct	gca	aaa	ttt	gac	att	acc	tct	gtt	gat	tat	gca	gaa	ttg	att	1298		
151	Lys	Pro	Ala	Lys	Phe	Asp	Ile	Thr	Ser	Val	Asp	Tyr	Ala	Glu	Leu	Ile			
152						420				425						430			
154	tat	gtg	att	cag	tcc	agg	gat	ttt	gaa	aaa	ggt	gtg	gag	att	gga	gta	1346		
155	Tyr	Val	Ile	Gln	Ser	Arg	Asp	Phe	Glu	Lys	Gly	Val	Glu	Ile	Gly	Val			
156						435				440						445			
158	tca	ttg	cct	aag	att	cat	atg	gat	gca	aaa	atc	ttt	gaa	gaa			1394		
159	Ser	Leu	Pro	Lys	Ile	His	Met	Asp	Ala	Phe	Ala	Lys	Ile	Phe	Glu	Glu			
160						450				455						460			
162	gdc	ttt	tgc	tct	ttg	tca	tagtctcttt	aatagaacca	tat	tttgctgc							1442		
163	Gly	Phe	Cys	Ser	Leu	Ser													
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166	aataaagtac	caagtccctt	agtaaacacta	caccaaacc	tactttcgag	gcccccaacac											1502		
168	cacaacgagg	ttcaatca	act	agaagg	ttgt	acttcataaa	ttccagaggt	cgaatataca									1562		
170	ccgttgtcct	ctgaaaagtt	gaac	cata	caca	cctgacatgg	tgttacgata	ggtattgtat									1622		
172	aatgccat	tata	acttcc	taa	agtatcc	tatgcaatag	agaacatgtt	atgtgttaaa									1682		
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192	atc	aaa	gtt	ctt	gag	aaa	tgc	cgt	gtt	gca	cca	ccg	gac	gcc	gtc		103		
193	Ile	Lys	Val	Leu	Glu	Lys	Cys	Arg	Val	Ala	Pro	Pro	Pro	Asp	Ala	Val			
194													10	15	20				
196	gcc	gag	ttt	aca	gtc	cca	ctg	tcg	ttt	tcc	gac	atg	cga	tgg	ttg	atc	151		

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201 Ser Asp Ala Glu His His Leu His Phe Tyr Arg Phe Arg His Pro Cys			
202 40	45	50	55
204 ccc aac tct aaa ttt atc att tca tcc att aaa tcg tcc ctt tcc ctt			247
205 Pro Asn Ser Lys Phe Ile Ile Ser Ser Ile Lys Ser Ser Leu Ser Leu			
206 60	65	70	
208 gtt ctc aaa cac ttt ctt ccg tta gcc ggg aat ttg att tgg ccg gta			295
209 Val Leu Lys His Phe Leu Pro Leu Ala Gly Asn Leu Ile Trp Pro Val			
210 75	80	85	
212 gat tcc tcc gat aga atg ccg gag ttg cgt tac aag aaa ggg gac tcc			343
213 Asp Ser Ser Asp Arg Met Pro Glu Leu Arg Tyr Lys Lys Gly Asp Ser			
214 90	95	100	
216 gtt tct tta aca att gca gaa tcg agc atg gat ttt gat tat ctc gcc			391
217 Val Ser Leu Thr Ile Ala Glu Ser Ser Met Asp Phe Asp Tyr Leu Ala			
218 105	110	115	
220 gga gat cat cag agg gat tct tat aaa ttc aac gat ttg att ccg cag			439
221 Gly Asp His Gln Arg Asp Ser Tyr Lys Phe Asn Asp Leu Ile Pro Gln			
222 120	125	130	135
224 ctg cca gaa ccg att gta acc tcc ggc gac gaa gta tta cca ctt ttt			487
225 Leu Pro Glu Pro Ile Val Thr Ser Gly Asp Glu Val Leu Pro Leu Phe			
226 140	145	150	
228 gct tta cag gtg acg gtg ttc tcc aac acc ggt ata tgc att gga cgc			535
229 Ala Leu Gln Val Thr Val Phe Ser Asn Thr Gly Ile Cys Ile Gly Arg			
230 155	160	165	
232 aat ctt cat caa gtt ctt ggt gat gcc agt tct ttt ctg cat ttt aat			583
233 Asn Leu His Gln Val Leu Gly Asp Ala Ser Ser Phe Leu His Phe Asn			
234 170	175	180	
236 aaa tta tgg gtt ttg gtt gac aaa tcc aat gga gat tca tta aag ttc			631
237 Lys Leu Trp Val Leu Val Asp Lys Ser Asn Gly Asp Ser Leu Lys Phe			
238 185	190	195	
240 ctt cca ctt tct tct cta cct atg tac gac aga tct gtg gtg caa gat			679
241 Leu Pro Leu Ser Ser Leu Pro Met Tyr Asp Arg Ser Val Val Gln Asp			
242 200	205	210	215
244 cca ttt cat att cgt cga aaa atc tac aat gaa aga aaa ctg ctc aaa			727
245 Pro Phe His Ile Arg Arg Lys Ile Tyr Asn Glu Arg Lys Leu Lys			
246 220	225	230	
248 tct cag ggc aca cct act gtt cta aat cca gca att tct aaa gat gaa			775
249 Ser Gln Gly Thr Pro Thr Val Leu Asn Pro Ala Ile Ser Lys Asp Glu			
250 235	240	245	
252 gtt cga gcc acc ttc atc cta cac cct att gat atc atg aag ctc aag			823
253 Val Arg Ala Thr Phe Ile Leu His Pro Ile Asp Ile Met Lys Leu Lys			
254 250	255	260	
256 aaa ttc att tcg tca aaa aat cgc aac tta acc ggt agt agt agt aat tat			871
257 Lys Phe Ile Ser Ser Lys Asn Arg Asn Leu Thr Gly Ser Ser Asn Tyr			
258 265	270	275	
260 aat ctg tca act ttc acg gtg aca tct gca ctg atc tgg aca tgc ttg			919
261 Asn Leu Ser Thr Phe Thr Val Thr Ser Ala Leu Ile Trp Thr Cys Leu			

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266																310	
267																	
268	cat	gca	gca	aac	tta	tgt	gct	ttc	atc	aac	tgc	cga	caa	cgt	ttt	gct	1015
269	His	Ala	Ala	Asn	Leu	Cys	Ala	Phe	Ile	Asn	Cys	Arg	Gln	Arg	Phe	Ala	
270																	
271																	
272	ccg	ccg	ata	cct	caa	aat	tac	ttt	gga	aat	tgc	ata	gtg	cct	tgt	atg	1063
273	Pro	Pro	Ile	Pro	Gln	Asn	Tyr	Phe	Gly	Asn	Cys	Ile	Val	Pro	Cys	Met	
274																	
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276	gtg	gga	tcg	act	cat	gag	caa	ttt	gta	gga	aat	gaa	ggg	ttg	tcg	gta	1111
277	Val	Gly	Ser	Thr	His	Glu	Gln	Leu	Val	Gly	Asn	Glu	Gly	Leu	Ser	Val	
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280	gct	gca	acc	gcc	atc	gga	gat	gct	atc	cat	aag	agg	tta	cat	gac	tac	1159
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284	gaa	gga	att	ctg	aga	gga	gat	tgg	ata	tcg	ccg	ccc	cga	tca	aca	tct	1207
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286																	
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288	gcg	gca	cca	agg	tcg	acg	ctc	att	tat	gtc	gtt	gga	tcc	gca	caa	cgc	1255
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292	aat	gtg	cat	gat	ttt	gat	ttt	ggt	tgg	gga	aag	ctt	gaa	aag		1303	
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294																	
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296	cat	gaa	tct	gtt	tca	act	aat	cct	tcg	gca	aca	cta	att	ttg	atc	tct	1351
297	His	Glu	Ser	Val	Ser	Thr	Asn	Pro	Ser	Ala	Thr	Leu	Ile	Leu	Ile	Ser	
298																	
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306																	
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/11/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:16; N Pos. 18
Seq#:22; N Pos. 9,15

VERIFICATION SUMMARY

PATENT APPLICATION: **US/08/894,356D**

DATE: 10/11/2005

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Input Set : **A:\72370308.app**

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L:1081 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0